



Figure 1A

1 GGAAGTCAGCAGCGCTTGGGAGGGGTGGCGGGGGAATAGCGGGCGCAGC
51 AGCCCCAGCCCTCAGAGACAGCAGAAAGGAGGGAGGGTGCTGG
101 GGGACAGCCCCCACCATTCTACCGCTATGGGCCCAACCTCCCACTCC
151 CACCTCCCCCTCATCGGCCGGGCTAGGACACCCCCCAAATCCCGTCGCCC
201 CCTTGACACGACACCCGACAGAGACAGAGACAGCCATCCGCCACCA
251 CCGCTGCCGAGCCTGGCTGGGAGGGGCCAGCCCCCAGGCCCCCTAC
301 CCCTCTGAGGTGGCCAGA ATG GAT TTG TGG CCA GGG GCA TGG
Met Asp Leu Trp Pro Gly Ala Trp
343 ATG CTG CTG CTG CTC TTC CTG CTG CTG CTC TTC C
Met Leu Leu Leu Leu Phe Leu Leu Leu Phe L
20
10
380 TG CTG CCC ACC CTG TGG TTC TGC AGC CCC AGT GCC AAG
eu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala Lys
30

Figure 1B

418 TAC TTC TTC AAG ATG GCC TTC TAC AAT GGC TGG ATC C
Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile L

40

455 TC TTC CTG GCT GTG CTC GCC ATC CCT GTG TGT GCC GTG
eu Phe Leu Ala Val Leu Ala Ile Pro Val Cys Ala Val

50

493 CGA GGA CGC AAC GTC GAG AAC ATG AAG ATC TTG CGT C
Arg Gly Arg Asn Val Glu Asn Met Lys Ile Leu Arg L

70

60

530 TA ATG CTG CTC CAC ATC AAA TAC CTG TAC GGG ATC CGA
eu Met Leu Leu His Ile Lys Tyr Leu Tyr Gly Ile Arg

80

Figure 1C

568 GTG GAG GTG CGA GGG GCT CAC CAC TTC CCT CCC TCG C
Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser G

90

605 AG CCC TAT GTT GTT GTC TCC AAC CAC CAG AGC TCT CTC
In Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu

100

643 GAT CTG CTT GGG ATG ATG GAG GTA CTG CCA GGC CGC T
Asp Leu Leu Gly Met Met Glu Val Leu Pro Gly Arg C

120

110

680 GT GTG CCC ATT GCC AAG CGC GAG CTA CTG TGG GCT GGC
ys Val Pro Ile Ala Lys Arg Glu Leu Leu Trp Ala Gly

130

Figure 1D

718 TCT GCC GGG CTG GCC TGC TGG CTG GCA GGA GTC ATC T
Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val Ile P

140

755 TC ATC GAC CGG AAG CGC ACG GGG GAT GCC ATC AGT GTC
he Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val

150

793 ATG TCT GAG GTC GCC CAG ACC CTG CTC ACC CAG GAC G
Met Ser Glu Val Ala Gln Thr Leu Leu Thr Gln Asp V

170

160

830 TG AGG GTC TGG GTG TTT CCT GAG GGA ACG AGA AAC CAC
al Arg Val Trp Val Phe Pro Glu Gly Thr Arg Asn His

180

Figure 1 E

868 AAT GGC TCC ATG CTG CCC TTC AAA CGT GGC GCC TTC C
Asn Gly Ser Met Leu Pro Phe Lys Arg Gly Ala Phe H
190

905 AT CTT GCA GTG CAG GCC CAG GTT CCC ATT GTC CCC ATA
is Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
200

943 GTC ATG TCC TCC TAC CAA GAC TTC TAC TGC AAG AAG G
Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys G
210 220

980 AG CGT CGC TTC ACC TCG GGA CAA TGT CAG GTG CGG GTG
lu Arg Arg Phe Thr Ser Gly Gln Cys Gln Val Arg Val
230

Figure 1F

1018 CTG CCC CCA GTG CCC ACG GAA GGG CTG ACA CCA GAT G
Leu Pro Pro Val Pro Thr Glu Gly Leu Thr Pro Asp A

240

1055 AC GTC CCA GCT CTG GCT GAC AGA GTC CGG CAC TCC ATG
sp Val Pro Ala Leu Ala Asp Arg Val Arg His Ser Met

250

1093 CTC ACT GTT TTC CGG GAA ATC TCC ACT GAT GGC CGG G
Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg G

270

260

1130 GT GGT GAC TAT CTG AAG AAG CCT GGG GGC GGT GGG
ly Gly Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly 280

1168 TGA ACCCTGGCTCTGAGCTCTCCTCCCATCTGTCCCCATCTTCTCTCCC

1216 CACACCTACCCACCCAGTGGGCCCTGAAGCAGGCCCAAACCCCTTCTCCTT

1266 GTCTCCCCCTCTCCCCACTTATCTCTCTCTTGTGGAATCTTCAACTTCTGAA

Figure 1G

1316 GTGAATGTGGATAACAGGCCACTCCTGCCCCCTCTTGGCCCCATCCATGG
1366 ACTCTTGCCCTCGGTGCAGTTTCCACTCTTGACCCCCACCTCCTACTGTCT
1416 TGTCTGTGGACAGTTGCCCTCCCCCTCATCTCCAGTGACTCAGCCTACAC
1466 AAGGAGGGGAACATTCCATCCCCAGTGGAGTCTCTTCCATATGTGTCTT
1516 CTCACCCCTCTACCCCCACATTGGCCAGTGGACTCATCCATTCTTTGGA
1566 ACAAAATCCCCCCTCCAAAGTCCATGGATTCAATGGACTCATCCATT
1616 TGTGAGGAGGACTTCTCGCCCTCTGGCTGGAGCTGATACCTGAAGCACT
1666 CCCAGGCTCATCCTGGGAGCTTTCCCTCAGCACCTTCACCTTCCCTCCCAG
1716 TGTAGCCTCCTGTCAAGTGGGGCTGGACCCCTTCTAATTCAGAGTCTCAT
1766 GCCTGCCCTTGCCAGATGCCCAGGGTCGTGCACTCTCTGGGATACCAGT
1816 TCAGTCTCCACATTTCTGTGGTTTCTGTCCCCATAGTACAGTTCTTCAGTG
1866 GACATGACCCCAACCAGCCCCCTGCAGCCCTGCTGACCATCTCACCAGAC
1916 ACAAGGGAAGAACAGACATCAGGTGCTGCACTCACTTCTGCCCCCTGG
1966 GGAGTTGGGAAAGGAACGAACCCCTGGCTGGAGGGGATAGGAGGCTTTT

Figure 1H

2016 AATTATTTCTTTTCTGTTGAGGCTTCCCCCTCTCTGAGCCAGTTTTC
2066 TTTCTTCCCTGGTGCAATTAGCCACTCCCTGCCTCTCACTCCAGACCTGTT
2116 CCCACAAC TGGGAGGTAGGCTGGGAGCAAAAGGAGAGGGTGGGACCCAG
2166 TTTTCCGTGGTTGGTTTATTAATTATCTGGATAACAGCAAAAACCTG
2216 AAAATAAGAGAGAGAGAAAAAAA

Figure 2 A

Human LPAAT	1	MDLWPGAWM-	10	20	30	40	50
Yeast LPAAT	1	MSV-IGREFLY	---	LLLLLF	LL-LLFLLP	LWFCSPSAKY	F-----FKMA
E.coli LPAAT	1	M-----	---	YLRSVL-VVL	AL-AG-----	---	-----C-----G
Maize LPAAT	1	MAI-----	---	PLVLVVL	PLGLLELLSG	LIVNAIQAVL	FVTIRPFESKS
Human LPAAT	51	FYNGWILFLA	60	70	80	90	100
Yeast LPAAT	51	FY-----G	---	VIASILCTLI	GKQHLAQWIT	ARCFYHVMKL	MLGLDV---K
E.coli LPAAT	51	-----	---	-----CLFS	PRNPKHVATF	GHMFGRLAPL	-FGLKVECRK
Maize LPAAT	51	FYRRINRFLA	EL-----	---	---	WLQLVWVVDW	WAGVKVQLHA
Human LPAAT	101	AHFE-PPSQ-	110	120	130	140	150
Yeast LPAAT	101	VUGE-ENLAK	---	KPYIMIANHQ	SSLDLLGMME	VL--PGRC--	-VPI-AKREL
E.coli LPAAT	101	PTDA-ESYG-	---	-NAIYIANHQ	STLDIFMLGR	IF--PPGCT-	---VTAKKSL
Maize LPAAT	101	DEETYSRMGK	EHALLISNHR	SDIDWL-IGW	ILAQRSGLG	IVQ-PP----	TVTIV-GKKSL
Human LPAAT	151	LWAGSAGLAC	160	170	180	190	200
Yeast LPAAT	151	KYVPFLG---	---	WFMALSGTYF	IDRKRTGDAL	SVMSEVAQTL	LTQDVRVWV-
E.coli LPAAT	151	LWIPFFGQLY	W----	LTGNLL	LDRSKRQEAI	DTLNKGLENV	KKNKRALWV-
Maize LPAAT	151	KFLPVIGWSM	WF----	AEYLF	IDRNNRTKAH	GTIAEVVNHF	KKRRISIWM-
Human LPAAT	201	FPEGTRNHN	GS-----	---	---	MLPFFKRGAFH	LAVQAQVPIV
Yeast LPAAT	201	FPEGTRSYT	SEL-----	---	---	MLPFFKRGAFH	LAQCKIPIV
E.coli LPAAT	201	FPEGTRSRG	RGL-----	---	---	-LPFKTGAFH	AAIAAGVPII
Maize LPAAT	201	LFEVGTRFTP	AKLLAAQEYA	ASQGLPAPRN	ILAPRTKGFV	SAVSIMRDFV	---

Figure 2 B

Human LPAAT	251	PIVMSSYQDF	YCKKERRFTS	GQCQVRVLPP	VPTEGLTPDD	VPALADR---
Yeast LPAAT	251	PVVVSNTSTL	VSPKYGVFNR	GCMIVRILKP	ISTENLTCKDK	IGEFAEK---
E.coli LPAAT	251	PVCVSTTSNK	I--NLNRLHN	GLVIVEMLPP	IDVSQYGKDQ	VRELAH---
Maize LPAAT	251	PAIYDTT--V	IVPKDSPQPT	MLRILKGQSS	VIHVRMKRHA	MSEMPKSD
		260	270	280	290	300
Human LPAAT	301	-----	VRHSM LT V-F	REISTDGRGG	GDYLKKPGGG	G*.....
Yeast LPAAT	301	-----	VRDQM VD T-L	KEIGYSPAIN	DTTLPPQ---	-----
E.coli LPAAT	301	-----	CRSIMEQK-I	AELDK EV AE-	-----	REAAKG V*.....
Maize LPAAT	301	VSKWCKDIFV	AKDALLDKHL	ATGTFDEEIR	PIGRPVKSLL	VTLFWSCLLL
		310	320	330	340	350
Human LPAAT	351
Yeast LPAAT	351	--AIEY---A	AL-----Q	HDKKVNKKIK	NEPVPSVIS	NDVNTHNEGS
E.coli LPAAT	351
Maize LPAAT	351	FGAIEFFKWT	QLLSTWRGVA	FTAAGMALVT	GVMHVFIMFS	QA-----ERS
		360	370	380	390	400
Human LPAAT	401
Yeast LPAAT	401	S-----V	KKMH*
E.coli LPAAT	401
Maize LPAAT	401	SSARAARNRV	KKE*
		410	420	430	440	450

Figure 3A

10	20	30	40	50	60
GGAGCGAGCT	GGCGGCGCCG	TCGGGCGCCG	GGCCGGGCCA	TGGAGCTGTG	GCCGTGTCTG
70	80	90	100	110	120
GCCGCGGCGC	TGCTGTTGCT	GCTGCTGCTG	GTGCAGCTGA	GCCGCGCGGC	CGAGTTCTAC
130	140	150	160	170	180
GCCAAGGTCTG	CCCTGTACTG	CGCGCTGTGC	TTCACGGTGT	CCGCCGTGGC	CTCGCTCGTC
190	200	210	220	230	240
TGCCTGCTGT	GCCACGGCGG	CCGGACGGTG	GAGAACATGA	GCATCATCGG	CTGGTTCTGTG
250	260	270	280	290	300
CGAAGCTTCA	AGTACTTTTA	CGGGCTCCGC	TTCGAGGTGC	GGGACCCGCG	CAGGCTGCAG
310	320	330	340	350	360
GAGGCCCGTC	CCTGTGTTCAT	CGTCTCCAAC	CACCAGAGCA	TCCTGGACAT	GATGGGCCCTC
370	380	390	400	410	420
ATGGAGGTCC	TTCCGGAGCG	CTGCGTGCAG	ATCGCCAAGC	GGGAGCTGCT	CTTCCTGGGG
430	440	450	460	470	480
CCCGTGGGCC	TCATCATGTA	CCTCGGGGGC	GTCCTTCTTCA	TCAACCGGCA	GCGCTCTAGC
490	500	510	520	530	540
ACTGCCATGA	CAGTGATGGC	CGACCTGGGC	GAGCGCATGG	TCAGGGAGAA	CCTCAAAGTG

Figure 3B

550	560	570	580	590	600
TGGATCTATC	CCGAGGGTAC	TCGCAACGAC	AATGGGACC	TGCTGCCTTT	TAAGAAGGCG
610	620	630	640	650	660
GCCTTCTACC	TGGCAGTCCA	GGCACAGGTG	CCCATCGTCC	CCGTGGTGTA	CTCTTCCTTC
670	680	690	700	710	720
TCCTCCTTCT	ACAACACCAA	GAAGAAGTTC	TTCACCTCAG	GAACAGTCAC	AGTGCAGGTG
730	740	750	760	770	780
CTGGAAGCCA	TCCCCACCAG	CGGCCTCACT	GCGGGGACG	TCCCTGGGCT	CGTGGACACC
790	800	810	820	830	840
TGCCACCGGG	CCATGAGGAC	CACCTTCCTC	CACATCTCCA	AGACCCCCCA	GGAGAACGGG
850	860	870	880	890	900
GCCACTGCGG	GGTCTGGCGT	GCAGCCGGCC	CAGTAGCCCA	GACCACGGCA	GGGCATGACC
910	920	930	940	950	960
TGGGGAGGGC	AGGTGGAAGC	CGATGGCTGG	AGGATGGCA	GAGGGGACTC	CTCCCCGGCTT
970	980	990	1000	1010	1020
CCAAATACCA	CTCTGTCCGG	CTCCCCCAGC	TCTCACTCAG	CCCGGAAGC	AGGAAGCCCC
1030	1040	1050	1060	1070	1080
TTCTGTCACT	GGTCTCAGAC	ACAGGCCCCCT	GGTGTCCCCT	GCAGGGGGCT	CAGCTGGACC

Figure 3C

1090	1100	1110	1120	1130	1140
CTCCCCGGC	TCGAGGGCAG	GGA CTGCGC	CCACGGCACC	TCTGGGNGCT	GGGNTGATAA
1150	1160	1170	1180	1190	1200
AGATGAGGCT	TGCGGCTGTG	GCCCCTGGT	GGGCTGAGCC	ACAAGGCCCC	CGATGGCCCA
1210	1220	1230	1240	1250	1260
GGAGCAGATG	GGAGGACCCC	GAGGCCAGGA	GTCCCAGACT	CACGCACCCT	GGGCCACAGG
1270	1280	1290	1300	1310	1320
GAGCCGGGAA	TCGGGGCCCTG	CTGCTCCTGC	TGGCCTGAAG	AATCTGTGGG	GTCAGCACTG
1330	1340	1350	1360	1370	1380
TACTCCGTTG	CTGTTTTTTT	ATAAACACAC	TCTTGGA AAA	AAAAA AAAA	AAAAA AAAA
1390	1400	1410	1420	1430	1440
AAA.....

Figure 4A

10	20	30	40	50
GGAGCGAGCTGGCGCGCGCTCGGCGCGCGCGCGGCC	ATG	GAG	CTG	TGG CCG
	Met	Glu	Leu	Trp Pro
60	70	80	90	
TGT CTG GCC GCG GCG CTG CTG TTG CTG CTG CTG	CTG	GAG	CTG	CAG CTG
Cys Leu Ala Ala Ala Leu Leu Leu Leu Leu	Leu	Val	Gln	Leu
10	20	30	40	50
100	110	120	130	140
AGC CGC GCG GCC GAG TTC TAC GCC AAG GTC GCC	CTG	TAC	TGC	GCG
Ser Arg Ala Ala Ala Glu Phe Tyr Ala Lys	Val	Ala	Leu	Tyr Cys Ala
30	40	50	60	
150	160	170	180	
CTG TGC TTC ACG GTG TCC GCC GTG GCC TCG	CTC	GTC	TGC	CTG CTG
Leu Cys Phe Thr Val Ser Ala Val Ala Ser	Leu	Val	Cys	Leu
40	50	60	70	
190	200	210	220	230
TGC CAC GGC GGC CCG ACG GTG GAG AAC	ATG	AGC	ATC	ATC GGC TGG
Cys His Gly Gly Arg Thr Val Glu Asn	Met	Ser	Ile	Ile Gly Trp
60	70	80	90	

Figure 4B

240	TTC GTG CGA AGC TTC AAG TAC TTT TAC GGG CTC CGC TTC GAG GTG	260	270	280
	Phe Val Arg Ser Phe Lys Tyr Phe Tyr Gly Leu Arg Phe Glu Val			80
		250		
		70		
280	290	300	310	320
CGG GAC CCG CGC AGG CTG CAG GAG GCC CGT CCC TGT GTC ATC GTC				
Arg Asp Pro Arg Arg Leu Gln Glu Ala Arg Pro Cys Val Ile Val				
				90
330	340	350	360	
TCC AAC CAC CAG AGC ATC CTG GAC ATG ATG GGC CTC ATG GAG GTC				
Ser Asn His Gln Ser Ile Leu Asp Met Met Gly Leu Met Glu Val				110
370	380	390	400	410
CTT CCG GAG CGC TGC GTG CAG ATC GCC AAG CGG GAG CTC CTC TTC				
Leu Pro Glu Arg Cys Val Gln Ile Ala Lys Arg Glu Leu Phe				
				120
420	430	440	450	
CTG GGG CCC GTG GGC CTC ATC ATG TAC CTC GGG GGC GTC TTC TTC				
Leu Gly Pro Val Gly Leu Ile Met Tyr Leu Gly Gly Val Phe Phe				140
460	470	480	490	500
ATC AAC CGG CAG CGC TCT AGC ACT GCC ATG ACA GTG ATG GCC GAC				
Ile Asn Arg Gln Arg Ser Thr Ala Met Thr Val Met Ala Asp				
				150

Figure 4C

510	520	530	540	
CTG GGC GAG CGC ATG GTC AGG GAG AAC CTC AAA GTG TGG ATC TAT				
Leu Gly Glu Arg Met Val Arg Glu Asn Leu Lys Val Trp Ile Tyr				170
160				
550	560	570	580	590
CCC GAG GGT ACT CGC AAC GAC AAT GGG GAC CTG CTG CCT TTT AAG				
Pro Glu Gly Thr Arg Asn Asp Asn Gly Asp Leu Leu Pro Phe Lys				
				180
600	610	620	630	
AAG GGC GCC TTC TAC CTG GCA GTC CAG GCA CAG GTG CCC ATC GTC				
Lys Gly Ala Phe Tyr Leu Ala Val Gln Ala Gln Val Pro Ile Val				200
190				
640	650	660	670	680
CCC GTG GTG TAC TCT TCC TTC TCC TCC TTC TAC AAC ACC AAG AAG				
Pro Val Val Tyr Ser Ser Phe Ser Ser Phe Tyr Asn Thr Lys Lys				
			210	
690	700	710	720	
AAG TTC TTC ACT TCA GGA ACA GTC ACA GTG CAG GTG CTG GAA GCC				
Lys Phe Phe Thr Ser Gly Thr Val Thr Val Gln Val Leu Glu Ala				230
				220

Figure 4 D

730 740 750 760 770
ATC CCC ACC AGC GGC CTC ACT GCG GCG GAC GTC CCT GCG CTC GTG
Ile Pro Thr Ser Gly Leu Thr Ala Ala Asp Val Pro Ala Leu Val
240

780 790 800 810
GAC ACC TGC CAC CCG GCC ATG AGG ACC ACC TTC CTC CAC ATC TCC
Asp Thr Cys His Arg Ala Met Arg Thr Thr Phe Leu His Ile Ser
250

820 830 840 850 860
AAG ACC CCC CAG GAG AAC GGG GCC ACT GCG GGG TCT GGC GTG CAG
Lys Thr Pro Gln Glu Asn Gly Ala Thr Ala Gly Ser Gly Val Gln
270

870 880 890 900 910 920
CCG GCC CAG TAG CCCAGACCAGGCAGGCATGACCTGGGGAGGCGAGGTGAAGC
Pro Ala Gln **

930 940 950 960 970 980
CGATGGCTGGAGGATGGGCAGAGGGGACTCCTCCCGGCTTCCAATACCACCTGTCCGG

990 1000 1010 1020 1030 1040
CTCCCCCAGCTCTCACTCAGCCCGGGAAGCAGGAAGCCCTTCTGTCACTGGTCTCAGAC
1050 1060 1070 1080 1090 1100
ACAGGCCCCGTGGTGTCCCCCTGCAGGGGGCTCAGCTGGACCCCTCCCGGGCTCGAGGCGAG

Figure 4 E

1110	1120	1130	1140	1150	1160
	GGACTCGCGCC	CACGGCACCTCTGGGNGCTGGNTGATAA	AGATGAGGCTT	CGCGCTGTG	
1170	1180	1190	1200	1210	1220
	GCCCGCTGGTGGCTGAGCCACAAGGCCCCCGATGGCC	CAGGAGCAGATGGGAGGACCCC			
1230	1240	1250	1260	1270	1280
	GAGGCCAGGAGTCCCAGACTCACGCACCCCTGGGCCACAGGAGCCGGGAAT	CGGGCCTG			
1290	1300	1310	1320	1330	1340
	CTGCTCCCTGCTGGCCTGAAGAA	TCTGTGGGT	CAGCAGTGTACTCCGTTGCTGTTTTTT		
1350	1360	1370	1380		
	ATAACACACTCTTGGAAAA	AAAAAAAAAAAAAAAAAAAA			

Figure 5 A

Alignment of LPAAT Sequences.

	10	20	30	40	50
Human LPAAT- β	1	---	---	MEL WPC---	LA AALLLLLV
Human LPAAT- α	1	---	---	MDL WPGAWLLLL	IFLLFLFLP
Yeast LPAAT	1	---	---	MSV --IGRFLYL	RSVLWLALA
E.coli LPAAT	1	---	---	---	---
H.influenzae	1	---	---	---	---
S.typhimurium	1	---	---	---	---
L.douglasi	1	MAKIRSS-L	RNR-----	RQLKP AVAATAD--D	DKDGVFMV--
C. nificera	1	MDASCASSFL	RGRCLESCFK	ASFGMSQPKD	AAGQPSRRPA DADDFIVDD
Human LPAAT- β	51	QL---	SRAAE FYAKVAL-YC	ALCFTVSAVA	SLVCLLCHGG RTVENM-SII
Human LPAAT- α	51	TLWFCSRSAK	YFFKMAF-YN	GWILFLAVLA	IPVCAV--RG RNVENM-KIL
Yeast LPAAT	51	G---CG---	FY-----	GVIA SILCTLIKQ	HLAQWI-TAR
E.coli LPAAT	51	---	MLYI FRLITVIYS	ILVC---VFG	SIYCLFSPRN PKHV---ATF
H.influenzae	51	---	MLKL LRIFLMLIC	ILIC---VLG	TIYSFIREKN PSNV---GIV
S.typhimurium	51	---	MLYI FRLITVIYS	ILVC---VFG	SIYCLFSPRN PKHV---ATF
L.douglasi	51	---	LLSC FKIFVCFAT	WLTAVANG	LIMVLLLPW YMRIRLGNLY
C. nificera	51	DRWTIVILSV	VRIAACFL--	SMWTTIVN	MIMVLLLPW YARIRQGNLY

Figure 5 B

	110	120	130	140	150
Human LPAAT- β	101 <u>GW</u> <u>VR</u> <u>SF</u> <u>KY</u> -	-- <u>FY</u> <u>GR</u> <u>FEV</u>	<u>RD</u> <u>PR</u> <u>RL</u> <u>Q</u> <u>EAR</u>	<u>PC</u> <u>VI</u> <u>VS</u> <u>NH</u> <u>Q</u> <u>S</u>	<u>I</u> <u>LD</u> <u>M</u> <u>G</u> <u>LM</u> <u>GL</u> <u>MEV</u>
Human LPAAT- α	101 <u>RL</u> <u>ML</u> <u>I</u> <u>HI</u> <u>KY</u> -	-- <u>LY</u> <u>G</u> <u>IR</u> <u>VEV</u>	<u>RG</u> <u>AH</u> <u>FP</u> <u>PS</u> <u>Q</u>	<u>PV</u> <u>VV</u> <u>VS</u> <u>NH</u> <u>Q</u> <u>S</u>	<u>S</u> <u>LD</u> <u>IL</u> <u>G</u> <u>MM</u> <u>EV</u>
Yeast LPAAT	101 <u>CFY</u> <u>-H</u> <u>VM</u> <u>KL</u> -	-- <u>ML</u> <u>GL</u> <u>D</u> <u>V</u> <u>KV</u>	<u>VGE</u> <u>EN</u> <u>LAK</u> <u>-K</u>	<u>PY</u> <u>IM</u> <u>IAN</u> <u>H</u> <u>Q</u> <u>S</u>	<u>T</u> <u>LD</u> <u>IF</u> <u>ML</u> <u>GR</u> <u>I</u>
E.coli LPAAT	101 <u>GH</u> <u>MF</u> <u>GRL</u> ---	<u>AP</u> <u>LF</u> <u>GL</u> <u>K</u> <u>VE</u> <u>C</u>	<u>RK</u> <u>PT</u> <u>DA</u> <u>ES</u> <u>Y</u> <u>G</u>	<u>NA</u> <u>IY</u> <u>IAN</u> <u>H</u> <u>Q</u> <u>N</u>	<u>NY</u> <u>DM</u> <u>VT</u> <u>AS</u> <u>NI</u>
H.influenzae	101 <u>AR</u> <u>WF</u> <u>GRL</u> <u>-FT</u>	<u>YPL</u> <u>F</u> <u>GL</u> <u>K</u> <u>VEH</u>	<u>RI</u> <u>PQ</u> <u>D</u> <u>Q</u> <u>K</u> <u>Q</u> <u>IS</u>	<u>RA</u> <u>IY</u> <u>IGN</u> <u>H</u> <u>Q</u> <u>N</u>	<u>NY</u> <u>DM</u> <u>VT</u> <u>IS</u> <u>YM</u>
S.typhimurii	101 <u>GH</u> <u>MF</u> <u>GRL</u> <u>-FT</u>	<u>AP</u> <u>LF</u> <u>GL</u> <u>K</u> <u>VE</u> <u>C</u>	<u>RK</u> <u>PA</u> <u>DA</u> <u>EN</u> <u>Y</u> <u>G</u>	<u>NA</u> <u>IY</u> <u>IAN</u> <u>H</u> <u>Q</u> <u>N</u>	<u>NY</u> <u>DM</u> <u>VT</u> <u>AN</u> <u>I</u>
L.douglasi	101 <u>CH</u> <u>II</u> <u>IG</u> <u>LV</u> --	<u>IW</u> <u>YG</u> <u>IP</u> <u>IK</u>	<u>QG</u> <u>SE</u> <u>HI</u> <u>K</u> <u>RA</u>	<u>IFT</u> <u>YI</u> <u>SN</u> <u>HA</u> <u>S</u>	<u>FI</u> <u>DA</u> <u>FF</u> <u>VM</u> <u>WL</u>
C.nucifera	101 <u>CH</u> <u>VT</u> <u>GR</u> <u>ML</u> <u>FT</u>	<u>MW</u> <u>IL</u> <u>GN</u> <u>PT</u> <u>IT</u>	<u>EG</u> <u>SE</u> <u>FS</u> <u>NI</u> <u>TR</u>	<u>I--YI</u> <u>CN</u> <u>HA</u> <u>S</u>	<u>LD</u> <u>IF</u> <u>IL</u> <u>IM</u> <u>WL</u>
	160	170	180	190	200
Human LPAAT- β	151 <u>LP</u> <u>ER</u> <u>CV</u> <u>Q</u> <u>IAK</u>	<u>RE</u> <u>LL</u> <u>FI</u> <u>GP</u> <u>V</u> -	<u>GL</u> <u>IM</u> <u>Y</u> <u>LG</u> <u>V</u>	<u>FF</u> <u>IN</u> <u>R</u> <u>Q</u> <u>RS</u> <u>ST</u>	<u>AM</u> <u>T--V</u> <u>MA</u> <u>LL</u>
Human LPAAT- α	151 <u>LP</u> <u>GR</u> <u>CV</u> <u>PIAK</u>	<u>RE</u> <u>LL</u> <u>W</u> <u>AG</u> <u>SA</u> -	<u>GL</u> <u>AC</u> <u>W</u> <u>L</u> <u>AG</u> <u>V</u>	<u>IF</u> <u>ID</u> <u>R</u> <u>K</u> <u>R</u> <u>T</u> <u>IGD</u>	<u>AI</u> <u>S--V</u> <u>M</u> <u>SEV</u>
Yeast LPAAT	151 <u>FP</u> <u>PG</u> <u>CT</u> <u>VTAK</u>	<u>KS</u> <u>LK</u> <u>V</u> <u>PF</u> <u>L</u> -	<u>GW</u> <u>F</u> <u>MA</u> <u>L</u> <u>SGT</u>	<u>YF</u> <u>LD</u> <u>R</u> <u>S</u> <u>K</u> <u>RQ</u> <u>E</u>	<u>AI</u> <u>D--T</u> <u>IN</u> <u>KG</u>
E.coli LPAAT	151 <u>VQ</u> <u>PT</u> <u>VT</u> <u>VGK</u>	<u>KS</u> <u>LL</u> <u>W</u> <u>IP</u> <u>FF</u> -	<u>GQ</u> <u>LY</u> <u>W</u> <u>L</u> <u>TGN</u>	<u>IL</u> <u>ID</u> <u>R</u> <u>NN</u> <u>R</u> <u>TK</u>	<u>AH</u> <u>G--T</u> <u>IA</u> <u>EV</u>
H.influenzae	151 <u>VQ</u> <u>PR</u> <u>IV</u> <u>SVGK</u>	<u>KS</u> <u>LI</u> <u>W</u> <u>IP</u> <u>FFF</u>	<u>TG</u> <u>LY</u> <u>W</u> <u>VTGN</u>	<u>IF</u> <u>LD</u> <u>EN</u> <u>R</u> <u>TK</u>	<u>AH</u> <u>N--T</u> <u>MS</u> <u>QL</u>
S.typhimurii	151 <u>VQ</u> <u>PT</u> <u>VT</u> <u>VGK</u>	<u>KS</u> <u>LL</u> <u>W</u> <u>IP</u> <u>FFF</u>	<u>TG</u> <u>Q</u> <u>LY</u> <u>W</u> <u>L</u> <u>TGN</u>	<u>IL</u> <u>ID</u> <u>R</u> <u>NN</u> <u>RAK</u>	<u>AH</u> <u>S--T</u> <u>IA</u> <u>AV</u>
L.douglasi	151 <u>AP</u> <u>IG</u> <u>TV</u> <u>GVAK</u>	<u>KE</u> <u>VI</u> <u>W</u> <u>YP</u> <u>ILG</u>	<u>Q--LY</u> <u>T</u> <u>LAH</u>	<u>IR</u> <u>ID</u> <u>RS</u> <u>NPAA</u>	<u>AI</u> <u>Q</u> <u>S</u> <u>FT</u> <u>M</u> <u>KEA</u>
C.nucifera	151 <u>IP</u> <u>K</u> <u>G</u> <u>TVT</u> <u>IAK</u>	<u>KE</u> <u>II</u> <u>W</u> <u>Y</u> <u>PLFG</u>	<u>Q</u> <u>FT</u> <u>LY</u> <u>V</u> <u>LANH</u>	<u>QR</u> <u>ID</u> <u>RS</u> <u>NP</u> <u>SA</u>	<u>AI</u> <u>ES--I</u> <u>KEV</u>

Figure 5C

Human LPAAT-β	201	GERMRENLK	210	220	230	240	250
Human LPAAT-α	201	AQTLLTQDVR	210	220	230	240	250
Yeast LPAAT	201	LENVKKNKRA	210	220	230	240	250
E.coli LPAAT	201	VNHFKKRRIS	210	220	230	240	250
H.influenzae	201	ARRINEDNLS	210	220	230	240	250
S.typhimurii	201	VNHFKKRRIS	210	220	230	240	250
L.douglassi	201	VRVITEKNLS	210	220	230	240	250
C. nucifera	201	ARAWKKNLS	210	220	230	240	250
Human LPAAT-β	251	VYSSFSS--F	260	270	280	290	300
Human LPAAT-α	251	VMSSYQD--F	260	270	280	290	300
Yeast LPAAT	251	VVSNTST--L	260	270	280	290	300
E.coli LPAAT	251	CVSTTS----	260	270	280	290	300
H.influenzae	251	VCSSTH----	260	270	280	290	300
S.typhimurii	251	CVSNTS----	260	270	280	290	300
L.douglassi	251	ILTGTHLAWF	260	270	280	290	300
C. nucifera	251	VLTGTHLAW-	260	270	280	290	300

Figure 5D

	310	320	330	340	350
Human LPAAT- β	301 <u>AMRTT</u> <u>FI</u> <u>HI</u> <u>S</u>	<u>K</u> <u>T</u> <u>P</u> <u>O</u> <u>E</u> <u>N</u> <u>G</u> <u>A</u> <u>T</u> <u>A</u>	<u>G</u> <u>S</u> <u>G</u> <u>V</u> <u>Q</u> <u>P</u> <u>A</u> <u>Q</u> *	-----	-----
Human LPAAT- α	301 <u>S</u> <u>M</u> <u>L</u> <u>T</u> <u>V</u> <u>F</u> <u>R</u> <u>E</u> <u>I</u> <u>S</u>	<u>T</u> <u>D</u> <u>C</u> <u>R</u> <u>G</u> <u>G</u> <u>D</u> <u>I</u> <u>L</u>	<u>K</u> <u>P</u> <u>G</u> <u>G</u> <u>G</u> *	-----	-----
Yeast LPAAT	301 <u>Q</u> <u>M</u> <u>V</u> <u>D</u> <u>I</u> <u>L</u> <u>K</u> <u>E</u> <u>I</u> <u>G</u>	<u>Y</u> <u>S</u> <u>P</u> <u>A</u> <u>I</u> <u>N</u> <u>D</u> <u>T</u> <u>T</u> <u>L</u>	<u>P</u> <u>P</u> <u>Q</u> <u>A</u> <u>I</u> <u>E</u> <u>Y</u> <u>A</u> <u>L</u>	<u>Q</u> <u>H</u> <u>D</u> <u>K</u> <u>K</u> <u>V</u> <u>N</u> <u>K</u> <u>I</u>	<u>K</u> <u>N</u> <u>E</u> <u>P</u> <u>V</u> <u>P</u> <u>S</u> <u>V</u> <u>S</u> <u>I</u>
E.coli LPAAT	301 - <u>S</u> <u>I</u> <u>M</u> <u>E</u> <u>Q</u> <u>K</u> <u>I</u> <u>A</u> <u>E</u>	<u>L</u> <u>D</u> <u>K</u> <u>E</u> <u>V</u> <u>A</u> — <u>E</u> <u>R</u>	<u>F</u> <u>A</u> <u>A</u> <u>C</u> <u>K</u> <u>V</u> *	-----	-----
H.influenzae	301 <u>T</u> <u>I</u> <u>L</u> <u>M</u> <u>E</u> <u>K</u> <u>R</u> <u>I</u> <u>A</u> <u>E</u>	<u>L</u> <u>D</u> <u>E</u> <u>E</u> <u>I</u> <u>A</u> -----	----- <u>K</u> <u>E</u> <u>N</u> *	-----	-----
S.typhimurii	301 <u>T</u> <u>A</u> <u>L</u> <u>M</u> <u>E</u> <u>Q</u> <u>K</u> <u>I</u> <u>A</u> <u>E</u>	<u>L</u> <u>D</u> <u>K</u> <u>E</u> <u>V</u> <u>A</u> — <u>E</u> <u>R</u>	<u>E</u> <u>A</u> <u>T</u> <u>G</u> <u>K</u> <u>V</u> *	-----	-----
L.douglasi	301 <u>I</u> <u>Y</u> <u>V</u> <u>R</u> <u>N</u> <u>L</u> <u>P</u> <u>A</u> <u>S</u> <u>Q</u>	<u>K</u> <u>P</u> <u>I</u> <u>G</u> <u>S</u> — <u>T</u> <u>N</u> <u>R</u>	— <u>S</u> — <u>K</u> *	-----	-----
C. nucifera	301 <u>T</u> <u>A</u> <u>L</u> <u>Y</u> <u>V</u> <u>D</u> <u>H</u> <u>L</u> <u>P</u> <u>E</u>	<u>S</u> <u>Q</u> <u>K</u> <u>P</u> <u>L</u> <u>N</u> <u>S</u> <u>K</u> <u>G</u> <u>R</u>	<u>D</u> <u>A</u> <u>S</u> <u>G</u> <u>R</u> <u>N</u> <u>S</u> *	-----	-----
	360	370	380	390	
Human LPAAT- β	351 -----	-----	-----	-----	-----
Human LPAAT- α	351 -----	-----	-----	-----	-----
Yeast LPAAT	351 <u>S</u> <u>N</u> <u>D</u> <u>V</u> <u>N</u> <u>T</u> <u>H</u> <u>N</u> <u>E</u> <u>G</u>	<u>S</u> <u>S</u> <u>V</u> <u>K</u> <u>K</u> <u>M</u> <u>H</u> *	-----	-----	-----
E.coli LPAAT	351 -----	-----	-----	-----	-----
H.influenzae	351 -----	-----	-----	-----	-----
S.typhimurii	351 -----	-----	-----	-----	-----
L.douglasi	351 -----	-----	-----	-----	-----
C. nucifera	351 -----	-----	-----	-----	-----

Figure 9 A

TCTATGAAACCAACATACATGGCGTTTGCATCACAGTTGGAGTCAGATGTGAGCCCGGAG	60
GGCAGGTGTCTGGCTTGTCACCCCGGAAGCCCTGAGGGCAGCTGTTCCCACTGGCTCTGC	120
TGACCTTGTGCCTTGGACGGCTGTCCTCAGCGAGGGGCCGTGCACCCGCTCCTGAGCAGC	180
GCC ATG GGC CTG CTG GCC TTC CTG AAG ACC CAG TTC GTG CTG CAC	225
Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His	
5 10	
CTG CTG GTC GGC TTT GTC TTC GTG GTG AGT GGT CTG GTC ATC AAC	270
Leu Leu Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn	
15 20 25	
TTC GTC CAG CTG TGC ACG CTG GCG CTC TGG CCG GTC AGC AAG CAG	315
Phe Val Gln Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln	
30 35 40	
CTC TAC CGC CGC CTC AAC TGC CGC CTC GCA TAC TCA CTC TGG AGC	360
Leu Tyr Arg Arg Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser	
45 50 55	
CAA CTG GTC ATG CTG CTG GAG TGG TGG TCC TGC ACG GAG TGT ACA	405
Gln Leu Val Met Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr	
60 65 70	
CTG TTC ACG GAC CAG GCC ACG GTA GAG CGC TTT GGG AAG GAG CAC	450
Leu Phe Thr Asp Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His	
75 80 85	
GCA GTC ATC ATC CTC AAC CAC AAC TTC GAG ATC GAC TTC CTC TGT	495
Ala Val Ile Ile Leu Asn His Asn Phe Glu Ile Asp Phe Leu Cys	
90 95 100	
GGG TGG ACC ATG TGT GAG CGC TTC GGA GTG CTG GGG AGC TCC AAG	540
Gly Trp Thr Met Cys Glu Arg Phe Gly Val Leu Gly Ser Ser Lys	
105 110 115	
GTC CTC GCT AAG AAG GAG CTG CTC TAC GTG CCC CTC ATC GGC TGG	585
Val Leu Ala Lys Lys Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp	
120 125 130	
ACG TGG TAC TTT CTG GAG ATT GTG TTC TGC AAG CGG AAG TGG GAG	630
Thr Trp Tyr Phe Leu Glu Ile Val Phe Cys Lys Arg Lys Trp Glu	
135 140 145	
GAG GAC CGG GAC ACC GTG GTC GAA GGG CTG AGG CGC CTG TCG GAC	675
Glu Asp Arg Asp Thr Val Val Glu Gly Leu Arg Arg Leu Ser Asp	
150 155 160	
TAC CCC GAG TAC ATG TGG TTT CTC CTG TAC TGC GAG GGG ACG CGC	720
Tyr Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu Gly Thr Arg	
165 170 175	
TTC ACG GAG ACC AAG CAC CGC GTT AGC ATG GAG GTG GCG GCT GCT	765
Phe Thr Glu Thr Lys His Arg Val Ser Met Glu Val Ala Ala Ala	
180 185 190	
AAG GGG CTT CCT GTC CTC AAG TAC CAC CTG CTG CCG CGG ACC AAG	810
Lys Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr Lys	
195 200 205	
GGC TTC ACC ACC GCA GTC AAG TGC CTC CGG GGG ACA GTC GCA GCT	855
Gly Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala	
210 215 220	
GTC TAT GAT GTA ACC CTG AAC TTC AGA GGA AAC AAG AAC CCG TCC	900
Val Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser	
225 230 235	
CTG CTG GGG ATC CTC TAC GGG AAG AAG TAC GAG GCG GAC ATG TGC	945
Leu Leu Gly Ile Leu Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys	
240 245 250	
GTG AGG AGA TTT CCT CTG GAA GAC ATC CCG CTG GAT GAA AAG GAA	990
Val Arg Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu	
255 260 265	
GCA GCT CAG TGG CTT CAT AAA CTG TAC CAG GAG AAG GAC GCG CTC	1035

Replacement Sheet
Appl. No.: 10/667,494
Title: HUMAN LYSOPHOSPHATIDIC ACID
ACYLTRANSFERASE GAMMA-1
POLYPEPTIDE (As Amended)
Inventors: David W. LEUNG *et al.*
Attv. Docket No.: 077319-0381

Figure 10A

CACGCTGGCGCTCTGGCCGGTCAGCAAGCAGCTCTACCGCCGCCTCAACTGCCGCCTCGCC	61
TACTCACTCTGGAGCCTAGCACAAAAGTAGAAGCAACCCCAAGCACCTGTCACTGGAGACT	121
AATTATGCGGCACCCATACAGGGACCCTCTGCGGCCATCATGGAGAGCCTTCATCTTGCC	181
CGTACAGTTTAAAGCGAAAAAGGAAGTATACAACAAAGTCCATAACTGGTC ATG CTG	238
	Met Leu
CTG GAG TGG TGG TCC TGC ACG GAG TGT ACA CTG TTC ACG GAC CAG	283
Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu Phe Thr Asp Gln	
5 10 15	
GCC ACG GTA GAG CGC TTT GGG AAG GAG CAC GCA GTC ATC ATC CTC	328
Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala Val Ile Ile Leu	
20 25 30	
AAC CAC AAC TTC GAG ATC GAC TTC CTC TGT GGG TGG ACC ATG TGT	373
Asn His Asn Phe Glu Ile Asp Phe Leu Cys Gly Trp Thr Met Cys	
35 40 45	
GAG CGC TTC GGA GTG CTG GGG AGC TCC AAG GTC CTC GCT AAG AAG	418
Glu Arg Phe Gly Val Leu Gly Ser Ser Lys Val Leu Ala Lys Lys	
50 55 60	
GAG CTG CTC TAC GTG CCC CTC ATC GGC TGG ACG TGG TAC TTT CTG	463
Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp Thr Trp Tyr Phe Leu	
65 70 75	
GAG ATT GTG TTC TGC AAG CGG AAG TGG GAG GAG GAC CGG GAC ACC	508
Glu Ile Val Phe Cys Lys Arg Lys Trp Glu Glu Asp Arg Asp Thr	
80 85 90	
GTG GTC GAA GGG CTG AGG CGC CTG TCG GAC TAC CCC GAG TAC ATG	553
Val Val Glu Gly Leu Arg Arg Leu Ser Asp Tyr Pro Glu Tyr Met	
95 100 105	
TGG TTT CTC CTG TAC TGC GAG GGG ACG CGC TTC ACG GAG ACC AAG	598
Trp Phe Leu Leu Tyr Cys Glu Gly Thr Arg Phe Thr Glu Thr Lys	
110 115 120	
CAC CGC GTT AGC ATG GAG GTG GCG GCT GCT AAG GGG CTT CCT GTC	643
His Arg Val Ser Met Glu Val Ala Ala Ala Lys Gly Leu Pro Val	
125 130 135	
CTC AAG TAC CAC CTG CTG CCG CGG ACC AAG GGC TTC ACC ACC GCA	688
Leu Lys Tyr His Leu Leu Pro Arg Thr Lys Gly Phe Thr Thr Ala	
140 145 150	
GTC AAG TGC CTC CGG GGG ACA GTC GCA GCT GTC TAT GAT GTA ACC	733
Val Lys Cys Leu Arg Gly Thr Val Ala Ala Val Tyr Asp Val Thr	
155 160 165	
CTG AAC TTC AGA GGA AAC AAG AAC CCG TCC CTG CTG GGG ATC CTC	778
Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu Leu Gly Ile Leu	
170 175 180	
TAC GGG AAG AAG TAC GAG GCG GAC ATG TGC GTG AGG AGA TTT CCT	823
Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys Val Arg Arg Phe Pro	
185 190 195	
CTG GAA GAC ATC CCG CTG GAT GAA AAG GAA GCA GCT CAG TGG CTT	868
Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala Ala Gln Trp Leu	
200 205 210	
CAT AAA CTG TAC CAG GAG AAG GAC GCG CTC CAG GAG ATA TAT AAT	913
His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln Glu Ile Tyr Asn	
215 220 225	
CAG AAG GGC ATG TTT CCA GGG GAG CAG TTT AAG CCT GCC CGG AGG	958
Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys Pro Ala Arg Arg	
230 235 240	
CCG TGG ACC CTC CTG AAC TTC CTG TCC TGG GCC ACC ATT CTC CTG	1003
Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala Thr Ile Leu Leu	
245 250 255	
TCT CCC CTC TTC AGT TTT GTC TTG GGC GTC TTT GCC AGC GGA TCA	1048
Ser Pro Leu Phe Ser Phe Val Leu Gly Val Phe Ala Ser Gly Ser	

Figure 10 B

	260		265		270		
CCT CTC CTG ATC CTG ACT TTC TTG GGG TTT GTG GGA GCA GCT TCC							1093
Pro Leu Leu Ile Leu Thr Phe Leu Gly Phe Val Gly Ala Ala Ser							
	275		280		285		
TTT GGA GTT CGC AGA CTG ATA GGA GTA ACT GAG ATA GAA AAA GGC							1138
Phe Gly Val Arg Arg Leu Ile Gly Val Thr Glu Ile Glu Lys Gly							
	290		295		300		
TCC AGC TAC GGA AAC CAA GAG TTT AAG AAA AAG GAA TAA TTAATGGC							1185
Ser Ser Tyr Gly Asn Gln Glu Phe Lys Lys Lys Glu ***							
	305		310				
TGTGACTGAACACACGCGGCCCTGACGGTGGTATCCAGTTAACTCAAAACCAACACACAG							1245
AGTGCAGGAAAAGACAATTAGAACTATTTTTCTTATTAAGTGGTGACTAATATTAACAA							1305
AACTTGAGCCAAGAGTAAAGAATTCAGAAGGCCTGTCAGGTGAAGTCTTCAGCCTCCCAC							1365
AGCGCAGGGTCCCAGCATCTCCACGCGCGCCCGTGGGAGGTGGGTCCGGCCGGAGAGGCC							1425
TCCCGCGGACGCGTCTCTCCAGAACTCCGCTTCCAAGAGGGACCTTTGGCTGCTTTCTC							1485
TCCTTAAACTTAGATCAAATTTTAAAAAAAAAAAAAAAA							1523

Figure 11A

TGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAAGGCTGCCAG	61
GAAGGAGACGCCTTCCTGAGTCCTGGATCTTTCTTCTCTGGAAATCTTTGACTGTGGG	121
TAGTTATTTATTTCTGAATAAGAGCGTCCACGCATC ATG GAC CTC GCG GGA CTG	175
Met Asp Leu Ala Gly Leu	
5	
CTG AAG TCT CAG TTC CTG TGC CAC CTG GTC TTC TGC TAC GTC TTT	220
Leu Lys Ser Gln Phe Leu Cys His Leu Val Phe Cys Tyr Val Phe	
10 15 20	
ATT GCC TCA GGG CTA ATC ATC AAC ACC ATT CAG CTC TTC ACT CTC	265
Ile Ala Ser Gly Leu Ile Ile Asn Thr Ile Gln Leu Phe Thr Leu	
25 30 35	
CTC CTC TGG CCC ATT AAC AAG CAG CTC TTC CGG AAG ATC AAC TGC	310
Leu Leu Trp Pro Ile Asn Lys Gln Leu Phe Arg Lys Ile Asn Cys	
40 45 50	
AGA CTG TCC TAT TGC ATC TCA AGC CAG CTG GTG ATG CTG CTG GAG	355
Arg Leu Ser Tyr Cys Ile Ser Ser Gln Leu Val Met Leu Leu Glu	
55 60 65	
TGG TGG TCG GGC ACG GAA TGC ACC ATC TTC ACG GAC CCG CGC GCC	400
Trp Trp Ser Gly Thr Glu Cys Thr Ile Phe Thr Asp Pro Arg Ala	
70 75 80	
TAC CTC AAG TAT GGG AAG GAA AAT GCC ATC GTG GTT CTC AAC CAC	445
Tyr Leu Lys Tyr Gly Lys Glu Asn Ala Ile Val Val Leu Asn His	
85 90 95	
AAG TTT GAA ATT GAC TTT CTG TGT GGC TGG AGC CTG TCC GAA CGC	490
Lys Phe Glu Ile Asp Phe Leu Cys Gly Trp Ser Leu Ser Glu Arg	
100 105 110	
TTT GGG CTG TTA GGG GGC TCC AAG GTC CTG GCC AAG AAA GAG CTG	535
Phe Gly Leu Leu Gly Gly Ser Lys Val Leu Ala Lys Lys Glu Leu	
115 120 125	
GCC TAT GTC CCA ATT ATC GGC TGG ATG TGG TAC TTC ACC GAG ATG	580
Ala Tyr Val Pro Ile Ile Gly Trp Met Trp Tyr Phe Thr Glu Met	
130 135 140	
GTC TTC TGT TCG CGC AAG TGG GAG CAG GAT CGC AAG ACG GTT GCC	625
Val Phe Cys Ser Arg Lys Trp Glu Gln Asp Arg Lys Thr Val Ala	
145 150 155	
ACC AGT TTG CAG CAC CTC CGG GAC TAC CCC GAG AAG TAT TTT TTC	670
Thr Ser Leu Gln His Leu Arg Asp Tyr Pro Glu Lys Tyr Phe Phe	
160 165 170	
CTG ATT CAC TGT GAG GGC ACA CGG TTC ACG GAG AAG AAG CAT GAG	715
Leu Ile His Cys Glu Gly Thr Arg Phe Thr Glu Lys Lys His Glu	
175 180 185	
ATC AGC ATG CAG GTG GCC CGG GCC AAG GGG CTG CCT CGC CTC AAG	760
Ile Ser Met Gln Val Ala Arg Ala Lys Gly Leu Pro Arg Leu Lys	
190 195 200	
CAT CAC CTG TTG CCA CGA ACC AAG GGC TTC GCC ATC ACC GTG AGG	805
His His Leu Leu Pro Arg Thr Lys Gly Phe Ala Ile Thr Val Arg	
205 210 215	
AGC TTG AGA AAT GTA GTT TCA GCT GTA TAT GAC TGT ACA CTC AAT	850
Ser Leu Arg Asn Val Val Ser Ala Val Tyr Asp Cys Thr Leu Asn	
220 225 230	
TTC AGA AAT AAT GAA AAT CCA ACA CTG CTG GGA GTC CTA AAC GGA	895
Phe Arg Asn Asn Glu Asn Pro Thr Leu Leu Gly Val Leu Asn Gly	
235 240 245	
AAG AAA TAC CAT GCA GAT TTG TAT GTT AGG AGG ATC CCA CTG GAA	940
Lys Lys Tyr His Ala Asp Leu Tyr Val Arg Arg Ile Pro Leu Glu	
250 255 260	
GAC ATC CCT GAA GAC GAT GAC GAG TGC TCG GCC TGG CTG CAC AAG	985
Asp Ile Pro Glu Asp Asp Asp Glu Cys Ser Ala Trp Leu His Lys	
265 270 275	

Figure 11 B